

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: HUMAN GENOME SCIENCES, INC.
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(ii) TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2

(iii) NUMBER OF SEQUENCES: 148

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US95/01790
(B) FILING DATE: 14-FEB-1995

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/461,195
(B) FILING DATE: 05-JUN-1995

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/023,852

(B) FILING DATE: 13-AUG-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/039,045
(B) FILING DATE: 28-FEB-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/862,432
(B) FILING DATE: 23-MAY-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/910,875
(B) FILING DATE: 13-AUG-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/055,561
(B) FILING DATE: 13-AUG-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1488.0360008/EKS

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG	48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
CCC GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC	96
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Phe Leu Val Ser Ser	
20 25 30	
GTC CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	

35	40	45	
GCC ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA			192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly			
50	55	60	
AGG CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA			240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg			
65	70	75	80
AAG CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG			288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly			
85	90	95	
AAG GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG			336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu			
100	105	110	
ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC			384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser			
115	120	125	
AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA			432
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys			
130	135	140	
GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA			480
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly			
145	150	155	160
TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG			528
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met			
165	170	175	
TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA			576
Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr			
180	185	190	
CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA			624
Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
195	200	205	
TAG			627

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Trp	Lys	Trp	Ile	Leu	Thr	His	Cys	Ala	Ser	Ala	Phe	Pro	His	Leu
1				5					10					15	
Pro	Gly	Cys	Cys	Cys	Cys	Cys	Phe	Leu	Leu	Phe	Leu	Val	Ser	Ser	
		20						25				30			
Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glu
		35					40					45			
Ala	Thr	Asn	Ser	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly
	50						55				60				
Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg
65					70					75					80
Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly
				85					90					95	
Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu
			100					105					110		
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
			115				120					125			
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys
			130				135				140				
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
145					150					155					160
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
				165					170					175	
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
			180					185					190		
Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser
			195				200					205			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCACATGT GGAAATGGAT ACTGACACAT TGTGCC

36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATGCCATGG CGTGCCAAGC CCTTGGTCAG GACATG

36

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGGATCCG CCATCATGTG GAAATGGATA CTCAC

35

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGCGGTACC ACAAACGTTG CCTTCCT

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAACGAGGAT CCGCCATCAT GTGGAAATGG ATACTGACAC

40

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAAGCACTCG AGTGAGTGTA CCACCATTGG AAGAAATG

38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTAACCCTC ACTAAGGGA GGCCATGTGG AAATGGATAC TGACACATTG TGCC

54

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCAAGCTTC CACAAACGTT GCCTTCCTCT ATGAG

35

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ser	Gly	Pro	Gly	Thr	Ala	Ala	Val	Ala	Leu	Leu	Pro	Ala	Val	Leu	1	5	10	15
Leu	Ala	Leu	Leu	Ala	Pro	Trp	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Ala	Pro	20	25	30	
Thr	Ala	Pro	Asn	Gly	Thr	Leu	Glu	Ala	Glu	Leu	Glu	Arg	Arg	Trp	Glu	35	40	45	
Ser	Leu	Val	Ala	Leu	Ser	Leu	Ala	Arg	Leu	Pro	Val	Ala	Ala	Gln	Pro	50	55	60	
Lys	Glu	Ala	Ala	Val	Gln	Ser	Gly	Ala	Gly	Asp	Tyr	Leu	Leu	Gly	Ile	65	70	75	80
Lys	Arg	Leu	Arg	Arg	Leu	Tyr	Cys	Asn	Val	Gly	Ile	Gly	Phe	His	Leu	85	90	95	
Gln	Ala	Leu	Pro	Asp	Gly	Arg	Ile	Gly	Gly	Ala	His	Ala	Asp	Thr	Arg	100	105	110	
Asp	Ser	Leu	Leu	Glu	Leu	Ser	Pro	Val	Glu	Arg	Gly	Val	Val	Ser	Ile	115	120	125	
Phe	Gly	Val	Ala	Ser	Arg	Phe	Phe	Val	Ala	Met	Ser	Ser	Lys	Gly	Lys	130	135	140	
Leu	Tyr	Gly	Ser	Pro	Phe	Phe	Thr	Asp	Glu	Cys	Thr	Phe	Lys	Glu	Ile	145	150	155	160
Leu	Leu	Pro	Asn	Asn	Tyr	Asn	Ala	Tyr	Glu	Ser	Tyr	Lys	Tyr	Pro	Gly	165	170	175	
Met	Phe	Ile	Ala	Leu	Ser	Lys	Asn	Gly	Lys	Thr	Lys	Lys	Gly	Asn	Arg	180	185	190	
Val	Ser	Pro	Thr	Met	Lys	Val	Thr	His	Phe	Leu	Pro	Arg	Leu	195	200	205			

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ser	Arg	Gly	Ala	Gly	Arg	Leu	Gln	Gly	Thr	Leu	Trp	Ala	Leu	Val	1	5	10	15
Phe	Leu	Gly	Ile	Leu	Val	Gly	Met	Val	Val	Pro	Ser	Pro	Ala	Gly	Thr	20	25	30	
Arg	Ala	Asn	Asn	Thr	Leu	Leu	Asp	Ser	Arg	Gly	Trp	Gly	Thr	Leu	Leu	35	40	45	
Ser	Arg	Ser	Arg	Ala	Gly	Leu	Ala	Gly	Glu	Ile	Ala	Gly	Val	Asn	Trp	50	55	60	
Glu	Ser	Gly	Tyr	Leu	Val	Gly	Ile	Lys	Arg	Gln	Arg	Arg	Leu	Tyr	Cys	65	70	75	80
Asn	Val	Gly	Ile	Gly	Phe	His	Leu	Gln	Val	Leu	Pro	Asp	Gly	Arg	Ile	85	90	95	
Ser	Gly	Thr	His	Glu	Glu	Asn	Pro	Tyr	Ser	Leu	Leu	Glu	Ile	Ser	Thr	100	105	110	
Val	Glu	Arg	Gly	Val	Val	Ser	Leu	Phe	Gly	Val	Arg	Ser	Ala	Leu	Phe	115	120	125	
Val	Ala	Met	Asn	Ser	Lys	Gly	Arg	Leu	Tyr	Ala	Thr	Pro	Ser	Phe	Gln	130	135	140	
Glu	Glu	Cys	Lys	Phe	Arg	Glu	Thr	Leu	Leu	Pro	Asn	Asn	Tyr	Asn	Ala	145	150	155	160
Tyr	Glu	Ser	Asp	Leu	Tyr	Gln	Gly	Thr	Tyr	Ile	Ala	Leu	Ser	Lys	Tyr	165	170	175	
Gly	Arg	Val	Lys	Arg	Gly	Ser	Lys	Val	Ser	Pro	Ile	Met	Thr	Val	Thr	180	185	190	
His	Phe	Leu	Pro	Arg	Ile	195													

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Ser	Leu	Ser	Phe	Leu	Leu	Leu	Leu	Phe	Phe	Ser	His	Leu	Ile	Leu	1	5	10	15
Ser	Ala	Trp	Ala	His	Gly	Glu	Lys	Arg	Leu	Ala	Pro	Lys	Gly	Gln	Pro	20	25	30	
Gly	Pro	Ala	Ala	Thr	Asp	Arg	Asn	Pro	Arg	Gly	Ser	Ser	Ser	Arg	Gln	35	40	45	
Ser	Ser	Ser	Ser	Ala	Met	Ser	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Pro	Ala	50	55	60	
Ala	Ser	Leu	Gly	Ser	Gln	Gly	Ser	Gly	Leu	Glu	Gln	Ser	Ser	Phe	Gln	65	70	75	80
Trp	Ser	Pro	Ser	Gly	Arg	Arg	Thr	Gly	Ser	Leu	Tyr	Cys	Arg	Val	Gly	85	90	95	
Ile	Gly	Phe	His	Leu	Gln	Ile	Tyr	Pro	Asp	Gly	Lys	Val	Asn	Gly	Ser	100	105	110	
His	Glu	Ala	Asn	Met	Leu	Ser	Val	Leu	Glu	Ile	Phe	Ala	Val	Ser	Gln	115	120	125	
Gly	Ile	Val	Gly	Ile	Arg	Gly	Val	Phe	Ser	Asn	Lys	Phe	Leu	Ala	Met	130	135	140	
Ser	Lys	Lys	Gly	Lys	Leu	His	Ala	Ser	Ala	Lys	Phe	Thr	Asp	Asp	Cys	145	150	155	160
Lys	Phe	Arg	Glu	Arg	Phe	Gln	Glu	Asn	Ser	Tyr	Asn	Thr	Tyr	Ala	Ser	165	170	175	
Ala	Ile	His	Arg	Thr	Glu	Lys	Thr	Gly	Arg	Glu	Trp	Tyr	Val	Ala	Leu	180	185	190	
Asn	Lys	Arg	Gly	Lys	Ala	Lys	Arg	Gly	Cys	Ser	Pro	Arg	Val	Lys	Pro	195	200	205	
Gln	His	Ile	Ser	Thr	His	Phe	Leu	Pro	Arg	Phe	Lys	Gln	Ser	Glu	Gln	210	215	220	
Pro	Glu	Leu	Ser	Phe	Thr	Val	Thr	Val	Pro	Glu	Lys	Lys	Asn	Pro	Pro	225	230	235	240
Ser	Pro	Ile	Lys	Ser	Lys	Ile	Pro	Leu	Ser	Ala	Pro	Arg	Lys	Asn	Thr	245	250	255	
Asn	Ser	Val	Lys	Tyr	Arg	Leu	Lys	Phe	Arg	Phe	Gly	260	265						

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
1           5           10           15
Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
20           25           30
Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
35           40           45
Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
50           55           60
Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
65           70           75           80
Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
85           90           95
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
100          105          110
Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
115          120          125
Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
130          135          140
Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
145          150          155
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
1           5           10           15

Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
          20           25           30

Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
          35           40           45

Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
          50           55           60

Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
65           70           75           80

Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
          85           90           95

Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
          100          105          110

Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
          115          120          125

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
          130          135          140

Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
145           150           155

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met Ala Pro Leu Gly Glu Val Gly Asn Tyr Phe Gly Val Gln Asp Ala
1           5           10           15

Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
          20           25           30

Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
          35           40           45

Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg

```

50	55	60
Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly		
65	70	75 80
Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu		
	85	90 95
Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser		
	100	105 110
Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu		
	115	120 125
Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp		
	130	135 140
Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg		
	145	150 155 160
Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr		
	165	170 175
Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val		
	180	185 190
Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser		
	195	200 205

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg		
1	5	10 15
Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys		
	20	25 30
Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser		
	35	40 45
Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile		

50		55		60
Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp				
65		70	75	80
Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn				
	85		90	95
Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly				
	100		105	110
Val Glu Ser Glu Phe Tyr Leu Ala Met Asn Lys Glu Gly Lys Leu Tyr				
	115		120	125
Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu				
	130		135	140
Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly				
145		150	155	160
Gly Glu Met ² Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly				
	165		170	175
Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala				
	180		185	190
Ile Thr				

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu			
1	5	10	15
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Phe Leu Val Ser Ser			
	20	25	30
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu			
	35	40	45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly			
	50	55	60

Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	
65						70				75					80	
Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	
			85						90					95		
Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	
			100					105					110			
Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	
			115				120					125				
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	
			130				135				140					
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	
145					150					155					160	
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	
				165					170					175		
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	
			180					185					190			
Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser	
			195				200					205				

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Gly	Leu	Ile	Trp	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Glu	Pro	Gly	Trp	
1				5					10					15		
Pro	Ala	Ala	Gly	Pro	Gly	Ala	Arg	Leu	Arg	Arg	Asp	Ala	Gly	Gly	Arg	
			20				25						30			
Gly	Gly	Val	Tyr	Glu	His	Leu	Gly	Gly	Ala	Pro	Arg	Arg	Arg	Lys	Leu	
		35					40					45				
Tyr	Cys	Ala	Thr	Lys	Tyr	His	Leu	Gln	Leu	His	Pro	Ser	Gly	Arg	Val	
	50					55					60					

Asn	Gly	Ser	Leu	Glu	Asn	Ser	Ala	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ala
65					70				75					80	
Val	Glu	Val	Gly	Ile	Val	Ala	Ile	Arg	Gly	Leu	Phe	Ser	Gly	Arg	Tyr
			85						90					95	
Leu	Ala	Met	Asn	Lys	Arg	Gly	Arg	Leu	Tyr	Ala	Ser	Glu	His	Tyr	Ser
			100					105					110		
Ala	Glu	Cys	Glu	Phe	Val	Glu	Arg	Ile	His	Glu	Leu	Gly	Tyr	Asn	Thr
		115					120					125			
Tyr	Ala	Ser	Arg	Leu	Tyr	Arg	Thr	Val	Ser	Ser	Thr	Pro	Gly	Ala	Arg
		130					135					140			
Arg	Gln	Pro	Ser	Ala	Glu	Arg	Leu	Trp	Tyr	Val	Ser	Val	Asn	Gly	Lys
145					150					155					160
Gly	Arg	Pro	Arg	Arg	Gly	Phe	Lys	Thr	Arg	Arg	Thr	Gln	Lys	Ser	Ser
					165				170					175	
Leu	Phe	Leu	Pro	Arg	Val	Leu	Asp	His	Arg	Asp	His	Glu	Met	Val	Arg
			180					185					190		
Gln	Leu	Gln	Ser	Gly	Leu	Pro	Arg	Pro	Pro	Gly	Lys	Gly	Val	Gln	Pro
		195					200					205			
Arg	Arg	Arg	Arg	Gln	Lys	Gln	Ser	Pro	Asp	Asn	Leu	Glu	Pro	Ser	His
		210					215				220				
Val	Gln	Ala	Ser	Arg	Leu	Gly	Ser	Gln	Leu	Glu	Ala	Ser	Ala	His	
225					230					235					

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Gly	Ser	Pro	Arg	Ser	Ala	Leu	Ser	Cys	Leu	Leu	Leu	His	Leu	Leu
1			5					10					15		
Val	Leu	Cys	Leu	Gln	Ala	Gln	Val	Arg	Ser	Ala	Ala	Gln	Lys	Arg	Gly
		20					25					30			
Pro	Gly	Ala	Gly	Asn	Pro	Ala	Asp	Thr	Leu	Gly	Gln	Gly	His	Glu	Asp

35	40	45
Arg Pro Phe Gly Gln Arg Ser Arg Ala Gly Lys Asn Phe Thr Asn Pro		
50	55	60
Ala Pro Asn Tyr Pro Glu Glu Gly Ser Lys Glu Gln Arg Asp Ser Val		
65	70	75
Leu Pro Lys Val Thr Gln Arg His Val Arg Glu Gln Ser Leu Val Thr		
	85	90
Asp Gln Leu Ser Arg Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg		
	100	105
Thr Ser Gly Lys His Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala		
	115	120
Met Ala Glu Asp Gly Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp		
	130	135
Thr Phe Gly Ser Arg Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr		
	145	150
Ile Cys Met Asn Lys Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys		
	165	170
Gly Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr		
	180	185
Ala Leu Gln Asn Ala Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg		
	195	200
Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu		
	210	215
Val His Phe Met Lys Arg Leu Pro Arg Gly His His Thr Thr Glu Gln		
	225	230
Ser Leu Arg Phe Glu Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu		
	245	250
Arg Gly Ser Gln Arg Thr Trp Ala Pro Glu Pro Arg		
	260	265

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 593..1216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA	60
CAACTCCAAA GGGATATACT TGTAGAAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA	120
CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC	180
CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTGTGGCA TCTAACATGG	240
TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA	300
CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA	360
CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG	420
CTTTTCCGAG GAGTTATGGA TGTGGTGCA TTTCACTTCTG GCCAGATCCG CGCCCAGAGG	480
GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT	540
CCAGTATGTT CCTTCTGATG AGACAATTTC CAGTGCCGAG AGTTTCAGTA CA ATG	595
	Met
	1
TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC	643
Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro	
5 10 15	
GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC	691
Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val	
20 25 30	
CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC	739
Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala	
35 40 45	
ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG	787
Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg	
50 55 60 65	
CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG	835
His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys	
70 75 80	
CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG	883
Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys	
85 90 95	
GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA	931
Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile	

100	105	110	
ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC			979
Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn			
115	120	125	
TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA			1027
Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu			
130	135	140	145
TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC			1075
Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr			
150	155	160	
AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT			1123
Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr			
165	170	175	
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA			1171
Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg			
180	185	190	
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA			1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser			
195	200	205	
TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG			1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC			1336
TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT			1396
AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT			1456
ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTTGTTGT TGTGTCAAG TTTTTGTTTT			1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG			1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT			1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTAAGGAAA GCACTTGGGT CATATCATAT			1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAATA			1756
TAAACATGTT AGTGTGAAAC TGTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC			1816
TGCCTTCATC CCTTCTATT TCTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT			1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG			1936
CACACCACAT GCATGTTTAC GACAAAGTGT TTTTAAACT TGGCGAACAC TTCAAAAATA			1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA			2056
CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG			2116

AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT	2296
TTCTTGCCAA ATGTCATGGC GGTAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416
CCCAGGGGCT TAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAACCAA ATAAACTTG TTTTCTGTAA	2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTAATAAGT TTAACCTTTG GAAATGCTGG CGTTCTGTGA	2896
TTCTCCAACA AACTTATTTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT	2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTCCC	3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTGA GGCAGTGTCT TTTGGCTTAT	3076
AGTTTAAATT GCATTTTCATC ATACTTTGCT TCCAACTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTGTG GTTGGAATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCTATCC AACTAGGTA TCTTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT	3376
TATTTACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCTGTCT CTCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TCGTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT	3796

GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA	4036
ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAAGA AAAAAAAG CAGTTTCAGC	4096
CCTGAATGTT GTAGATTGTA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA	4156
TTCGCCCTAT AGTGAGTCGT A	4177

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	1	5	10	15
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	20	25	30	
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	35	40	45	
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly	50	55	60	
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	65	70	75	80
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	85	90	95	
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	100	105	110	
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	115	120	125	
Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	130	135	140	
Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	145	150	155	160

Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met
165 170 175

Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr
180 185 190

Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser
1 5 10 15

Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys
1 5 10 15

Pro Tyr Ser

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys
1				5					10					15	
Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr		
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn
1				5				10						15	
Thr	Ser	Ala													

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATG AGA GGA TCG CAT CAC CAT CAC CAT CAC GGA TCC TGC CAG GCT CTG	48
Met. Arg Gly Ser His His His His His His Gly Ser Cys Gln Ala Leu	
1 5 10 15	
GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC AAC TCT TCC TCT TCC TCT	96
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser	
20 25 30	
TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC	144
Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His	
35 40 45	
CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC	192
Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr	
50 55 60	
TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG	240
Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu	
65 70 75 80	
AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT	288
Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val	
85 90 95	
GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG	336
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys	
100 105 110	
AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG	384
Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu	
115 120 125	
AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC	432
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
130 135 140	
TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA	480
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
145 150 155 160	
GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC	528
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
165 170 175	
TTT CTT CCA ATG GTG GTA CAC TCA TAG	555
Phe Leu Pro Met Val Val His Ser	
180	

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

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Met Arg Gly Ser His His His His His Gly Ser Cys Gln Ala Leu
 1           5           10           15
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser
 20           25           30
Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His
 35           40           45
Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr
 50           55           60
Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu
 65           70           75           80
Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val
 85           90           95
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys
100           105           110
Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu
115           120           125
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn
130           135           140
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly
145           150           155           160
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His
165           170           175
Phe Leu Pro Met Val Val His Ser
180

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGTGGAAAT GGATACTGAC CCACTGCGCT TCTGCTTTCC CGCACCTGCC GGGTTGCTGC 60

TGCTGCTGCT TCCTGCTGCT GTTC 84

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCGGAGAAAC CATGTCCTGA CCCAGAGCCT GGCAGGTAAC CGGAACAGAA GAAACCAGGA 60

ACAGCAGCAG GAAGCAGCAG CA 82

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGGTCAGGAC ATGTTTTCTC CGGAAGCTAC CAACTCTTCT TCTTCTTCTT TCTTTCTCC 60

GTCTTCTGCT GGTCGTCACG 80

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTGAAAGAG AACAGTTTAC GCCAACGAAC GTCACCCTGC AGGTGGTTGT AAGAACGAAC 60
GTGACGACCA GCAGAAGACG G 81

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CGTTGGCGTA AACTGTTCTC TTTCACCAAA TACTTCCTGA AAATCGAAAA AAACGGTAAA 60
GTTTCTGGGA CCAA 75

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTTGGTCCCA GAAACTTTAC CGTTTTTTTC GATTTTCAG 39

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAAGGATCCA TGTGGAAATG GATACTGACC CACTGC

36

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG TGG AAA TGG ATA CTG ACC CAC TGC GCT TCT GCT TTC CCG CAC CTG	48
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	
1 5 10 15	
CCG GGT TGC TGC TGC TGC TGC TTC CTG CTG CTG TTC CTG GTT TCT TCT	96
Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	
20 25 30	
GTT CCG GTT ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA	144
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	
35 40 45	
GCT ACC AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG ACT TCC GCT GGT	192
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly	
50 55 60	
CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT	240
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	
65 70 75 80	
AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT	288
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	
85 90 95	
AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG	336
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	
100 105 110	
ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC	384
Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	
115 120 125	

AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys 130 135 140	432
GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly 145 150 155 160	480
TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met 165 170 175	528
TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr 180 185 190	576
CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser 195 200 205	624
TAG	627

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu 1 5 10 15
Pro Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser 20 25 30
Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu 35 40 45
Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Thr Ser Ala Gly 50 55 60
Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg 65 70 75 80
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly 85 90 95
Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu 100 105 110

Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
		115					120						125		
Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys
	130					135					140				
Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
145					150					155					160
Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
				165					170					175	
Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
			180					185					190		
Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTCATGACT TGTCAAGCTC TGGGTCAAGA TATGGTTC

38

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCCCAAGCTT CCACAAACGT TGCCTTCC

28

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160

AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA 522
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

TAG 525

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
1 5 10 15
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
20 25 30
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
35 40 45
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
50 55 60
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
65 70 75 80
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
85 90 95
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
100 105 110
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
115 120 125
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
130 135 140
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
145 150 155 160
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCAGTGAATT CATTAAAGAG GAGAAATTAA TCATGACTTG CCAGG

45

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCATGACTTG CCAGGCACTG GGTCAAGACA TGGTTTCCCC GGAAGCTA

48

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCTTCAGCAG CCCATCTAGC GCAGGTCGTC ACGTTCGCTC TTACAACC

48

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTCGTTGGC GCAAACTGTT CAGCTTTACC AAGTACTTCC TGAAAATC

48

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCGAAAAAAA CGGTAAAGTT TCTGGGAC

28

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGGGCTGC TGAAGCTAGA GCTGGAGCTG TTGGTAGCTT CCGGGGAA

48

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AACAGTTTGC GCCAACGAAC ATCACCTGT AAGTGGTTGT AAGAG

45

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTCTTGGTCC CAGAACTTT ACCGTTTTTT TCGATTTTCA GGAAGTA

47

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TTCTTGGTCC CAGAACTTT ACCG

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGATCAGGCT TCTATTATTA TGAGTGTACC ACCATTGGAA GAAAG

45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATG ACT TGC CAG GCA CTG GGT CAA GAC ATG GTT TCC CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC AGC TCC AGC TCT AGC TTC AGC AGC CCA TCT AGC GCA GGT CGT CAC	96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGC TCT TAC AAC CAC TTA CAG GGT GAT GTT CGT TGG CGC AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC AGC TTT ACC AAG TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg	
145 150 155 160	
AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	522
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
165 170	
TAG	525

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg	

145	150	155	160
Lys	Asn	Thr	Ser
Ala	His	Phe	Leu
Pro	Met	Val	Val
His	Ser		
165	170		

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGACCCTCAT GACCTGCCAG GCTCTGGGTC AGGAC 35

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGACAGCCAT GGCTGGTCGT CACGTTTCG 28

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGACAGCCAT GGTTTCGTTGG CGTAAACTG 29

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGACAGCCAT GGAAAAAAC GGTAAGTTT C

31

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGACCCCCAT GGAGAACTGC CCGTAGAGC

29

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGACCCCCAT GGTCAAAGCC ATTAACAGCA AC

32

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGACCCCCAT GGGGAAACTC TATGGCTCAA AAG

33

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTGCCCAAGC TTATTATGAG TGTACCACCA TTGGAAG

37

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTGCCCAAGC TTATTACTTC AGCTTACAGT CATTGT

36

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC TAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT	384
Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn	
115 120 125	
ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG	432
Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val	
130 135 140	
GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG	480
Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg	
145 150 155 160	
AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	522
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
165 170	
TAG	525

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr
 1              5              10              15

Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His
      20              25              30

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
      35              40              45

Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
      50              55              60

Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
      65              70              75              80

Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
      85              90              95

Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
      100              105              110

Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn
      115              120              125

Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val
      130              135              140

Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg
      145              150              155              160

Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
      165              170

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(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATG GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT	48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val	
1 5 10 15	
CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA	96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu	
20 25 30	
AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC	144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser	
35 40 45	
ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC	192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala	
50 55 60	
ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT	240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr	
65 70 75 80	
GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG	288
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu	
85 90 95	
GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG	336
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly	
100 105 110	
AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA	384
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly	
115 120 125	
CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG	432
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val	
130 135 140	
GTA CAC TCA TAG	444
Val His Ser	
145	

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu
85 90 95
Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly
100 105 110
Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly
115 120 125
Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val
130 135 140
Val His Ser
145

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ATG GTT CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA
Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys
1 5 10 15

ATC GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro 20 25 30	96
TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val 35 40 45	144
AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys 50 55 60	192
CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg 65 70 75 80	240
ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His 85 90 95	288
AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg 100 105 110	336
AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro 115 120 125	384
ATG GTG GTA CAC TCA TAG Met Val Val His Ser 130	402

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys 1 5 10 15
Ile Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro 20 25 30
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val 35 40 45
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys 50 55 60

Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg
65 70 75 80

Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His
85 90 95

Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg
100 105 110

Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro
115 120 125

Met Val Val His Ser
130

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATG GAA AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG	48
Met Glu Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro	
1 5 10 15	
TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC	96
Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val	
20 25 30	
AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA	144
Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys	
35 40 45	
CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG	192
Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg	
50 55 60	
ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT	240
Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His	
65 70 75 80	
AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG	288
Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg	

	85	90	95	
AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA				336
Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro				
	100	105	110	
ATG GTG GTA CAC TCA TAG				354
Met Val Val His Ser				
	115			

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Glu	Lys	Asn	Gly	Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	
1				5					10					15		
Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	
			20					25					30			
Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	
			35				40					45				
Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	
	50					55				60						
Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	
65					70				75					80		
Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	
				85					90					95		
Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	
			100					105					110			
Met	Val	Val	His	Ser												
			115													

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA TCA GTA GAA ATC	48
Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile	
185 190 195 200	
GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT TAC TTA GCC ATG	96
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met	
205 210 215	
AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT AAC AAT GAC TGT	144
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys	
220 225 230	
AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA	192
Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser	
235 240 245	
TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA	240
Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly	
250 255 260	
AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT	288
Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser	
265 270 275 280	
GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA TAG	321
Ala His Phe Leu Pro Met Val Val His Ser	
285 290	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile	
1 5 10 15	
Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met	
20 25 30	
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys	

(2) INFORMATION FOR SEQ ID NO:75:

(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..261

[illegible]

Leu Pro Met Val Val His Ser
85

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	
1					5				10					15		
Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	
			20					25					30			
Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	
			35				40					45				
Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	
	50					55					60					
Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	
	65				70					75					80	
Leu	Pro	Met	Val	Val	His	Ser										
					85											

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATG	GGG	AAA	CTC	TAT	GGC	TCA	AAA	GAA	TTT	AAC	AAT	GAC	TGT	AAG	CTG	
Met	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	
1					5				10					15		

AAG GAG AGG ATA GAG GAA AAT GGA TAC AAT ACC TAT GCA TCA TTT AAC	96
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
20 25 30	
TGG CAG CAT AAT GGG AGG CAA ATG TAT GTG GCA TTG AAT GGA AAA GGA	144
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
35 40 45	
GCT CCA AGG AGA GGA CAG AAA ACA CGA AGG AAA AAC ACC TCT GCT CAC	192
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
50 55 60	
TTT CTT CCA ATG GTG GTA CAC TCA TAG	219
Phe Leu Pro Met Val Val His Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu	
1 5 10 15	
Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn	
20 25 30	
Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn Gly Lys Gly	
35 40 45	
Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His	
50 55 60	
Phe Leu Pro Met Val Val His Ser	
65 70	

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

ATG ACC TGC CAG GCT CTG GGT CAG GAC ATG GTT TCT CCG GAA GCT ACC	48
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
AAC TCT TCC TCT TCC TCT TTC TCT TCC CCG TCT TCC GCT GGT CGT CAC	96
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	
GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT CGT TGG CGT AAA CTG	144
Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu	
35 40 45	
TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA AAA AAC GGT AAA GTT	192
Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val	
50 55 60	
TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA ACA	240
Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr	
65 70 75 80	
TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC TAT	288
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr	
85 90 95	
TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA TTT	336
Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe	
100 105 110	
AAC AAT GAC TGT AAG CTG AAG	357
Asn Asn Asp Cys Lys Leu Lys	
115	

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr	
1 5 10 15	
Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His	
20 25 30	

Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu
 35 40 45
 Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val
 50 55 60
 Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr
 65 70 75 80
 Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr
 85 90 95
 Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe
 100 105 110
 Asn Asn Asp Cys Lys Leu Lys
 115

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATG GCT GGT CGT CAC GTT CGT TCT TAC AAC CAC CTG CAG GGT GAC GTT	48
Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val	
1 5 10 15	
CGT TGG CGT AAA CTG TTC TCT TTC ACC AAA TAC TTC CTG AAA ATC GAA	96
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu	
20 25 30	
AAA AAC GGT AAA GTT TCT GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC	144
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser	
35 40 45	
ATC CTG GAG ATA ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC	192
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala	
50 55 60	
ATT AAC AGC AAC TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT	240
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr	
65 70 75 80	

GGC TCA AAA GAA TTT AAC AAT GAC TGT AAG CTG AAG
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
85 90

276

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val
1 5 10 15
Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu
20 25 30
Lys Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser
35 40 45
Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala
50 55 60
Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr
65 70 75 80
Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys
85 90

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGACCTCTC AGGCTCTGGG TCAGGACATG GTTTCTCCGG AAGCTACCAA CTCTTCCTCT 60
TCCTCTTTCT CTTCCCCGTC TTCCGCTGGT CGTCACGTTT GTTCTTACAA CCACCTGCAG 120
GGTGACGTTT GTTGGCGTAA ACTGTTCTCT TTCACCAAT ACTTCCTGAA AATCGAAAAA 180

AACGGTAAAG TTTCTGGGAC CAAGAAGGAG AACTCTCCGT ACAGCATCCT GGAGATAACA	240
TCAGTAGAAA TCGGAGTTGT TGCCGTCAAA GCCATTAACA GCAACTATTA CTTAGCCATG	300
AACAAGAAGG GGAAACTCTA TGGCTCAAAA GAATTTAACA ATGACTGTAA GCTGAAGGAG	360
AGGATAGAGG AAAATGGATA CAATACCTAT GCATCATTTA ACTGGCAGCA TAATGGGAGG	420
CAAATGTATG TGGCATTGAA TGGAAAAGGA GCTCCAAGGA GAGGACAGAA AACACGAAGG	480
AAAAACACCT CTGCTCACTT TCTTCCAATG GTGGTACACT CATAG	525

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGACCTGCC AGGCTCTGGG TCAGGACATG GTTCTCCGG AAGCTACCAA CTCTTCCTCT	60
TCCTCTTTCT CTTCCCCGTC TTCCGCTGGT CGTCACGTTT GTTCTTACAA CCACCTGCAG	120
GGTGACGTTT GTTGGCGTAA ACTGTTCTCT TTCACCAAAT ACTTCTGAA AATCGAAAAA	180
AACGGTAAAG TTTCTGGGAC CAAGAAGGAG AACTCTCCGT ACAGCATCCT GGAGATAACA	240
TCAGTAGAAA TCGGAGTTGT TGCCGTCAAA GCCATTAACA GCAACTATTA CTTAGCCATG	300
AACAAGAAGG GGAAACTCTA TGGCTCAAAA GAATTTAACA ATGACTGTAA GCTGAAGGAG	360
AGGATAGAGG AAAATGGATA CAATACCTAT GCATCATTTA ACTGGCAGCA TAATGGGAGG	420
CAAATGTATG TGGCATTGAA TGGAAAAGGA GCTCCAAGGA GAGGACAGAA AACACGAAGG	480
AAAAACACCT CTGCTCACTT TCTTCCAATG GTGGTACACT CATAG	525

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGACCCTCAT GACCTCTCAG GCTCTGGGT

29

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGAGAACT CTCCGTACAG C

21

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GCTGTACGGT CTGTTCTCCT T

21

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGACCCTCAT GACCTGCCAG GCTCTGGGTC AGGAC

35

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCCCAAGC TTATTATGAG TGTACCACCA TTGGAAG

37

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AAAGGATCCT GCCAGGCTCT GGGTCAGGAC ATG

33

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGGCCCAAGC TTATGAGTGT ACCACCAT

28

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

CCGGCGGATC CCATATGTCT TACAACCACC TGCAGG

36

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCGGCGGTAC CTTATTATGA GTGTACCACC ATTGG

35

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA	60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCCTGGGA CCAAGAAGGA GAACTGCCCCG	120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG	360
AGAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAA	426

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe	
1 5 10 15	
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser	
20 25 30	
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser	
35 40 45	
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr	
50 55 60	
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn	
65 70 75 80	

Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr
				85					90					95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala
			100					105					110		
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys
			115				120					125			
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser			
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CAACCACCTG CAGGGTGACG

20

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AACGGTCGAC AAATGTATGT GGCACCTGAAC GGTAAGGTTG CTCCACGTCG TGGTCAGAAA

60

ACCCGTCGTA AAAACACC

78

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GGGCCCCAAGC TTAAGAGTGT ACCACCATTG GCAGAAAGTG AGCAGAGGTG TTTTACGAC 60

GGGTTTTCTG ACCACG 76

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCCACATACA TTTGTCGACC GTT 23

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGGCCCCAAGC TTAAGAGTG 19

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCCACATACA TTTGTCGACC GTT

23

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTGCAGGGTG ACGTTCGTTG GCGTAAACTG TTCTCCTTCA CCAAATACTT CCTGAAAATC

60

GAAAAAAACG GTAAAGTTTC TGGTACCAAG

90

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AGCTTTAACA GCAACAACAC CGATTTCAAC GGAGGTGATT TCCAGGATGG AGTACGGGCA

60

GTTTTCTTTC TTGGTACCAG AAACTTTACC

90

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGTGTGTGTTG CTGTTAAAGC TATCAACTCC AACTACTACC TGGCTATGAA CAAGAAAGGT 60
AAACTGTACG GTTCCAAAGA ATTTAACAAC 90

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCGACCGTT GTGCTGCCAG TTGAAGGAAG CGTAGGTGTT GTAACCGTTT TCTTCGATAC 60
GTTCTTTCAG TTTACAGTCG TTGTTAAATT CTTTGAACC 100

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCGGCGTCGA CCGTTGTGCT GCCAG 25

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

1005445 "01503
205429"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCGGCCTGCA GGGTGACGTT CGTTGG

26

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CCGGCGGATC CCATATGTCT TACAACCACC TGCAGG

36

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CGGCGGATAT CTTATTAAGA GTGTACCACC ATTG

34

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC CTTACCAAA

60

2025-04-04 10:44:04

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGTA CCAAGAAAGA AACTGCCCCG 120
TACTCCATCC TGGAAATCAC CTCCGTTGAA ATCGGTGTTG TTGCTGTTAA AGCTATCAAC 180
TCCAACACT ACTGCGCTAT GAACAAGAAA GGTAAGTGT ACGGTTCCAA AGAATTTAAC 240
AACGACTGTA AACTGAAAGA ACGTATCGAA GAAAACGGTT ACAACACCTA CGCTTCCTTC 300
AACTGGCAGC ACAACGGTCG ACAAATGTAT GTGGCACTGA ACGGTAAAGG TGCTCCACGT 360
CGTGGTCAGA AAACCCGTCG TAAAAACACC TCTGCTCACT TTCTGCCAAT GGTGGTACAC 420
TCTTAA 426

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CGCGGCCATG GCTCTGGGTC AGGACATG

28

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GGGCCCAAGC TTATGAGTGT ACCACCAT

28

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATGGCTCTGG GTCAAGATAT GGTTCCTCCG GAAGCTACCA ACTCTTCCTC TTCCTCTTTC	60
TCTTCCCCGT CTTCCGCTGG TCGTCACGTT CGTTCTTACA ACCACCTGCA GGGTGACGTT	120
CGTTGGCGTA AACTGTTCTC TTTCACCAAA TACTTCCTGA AAATCGAAAA AAACGGTAAA	180

GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG TACAGCATCC TGGAGATAAC ATCAGTAGAA 240
 ATCGGAGTTG TTGCCGTCAA AGCCATTAAAC AGCAACTATT ACTTAGCCAT GAACAAGAAG 300
 GGGAAACTCT ATGGCTCAAA AGAATTTAAC AATGACTGTA AGCTGAAGGA GAGGATAGAG 360
 GAAAATGGAT ACAATACCTA TGCATCATTT AACTGGCAGC ATAATGGGAG GCAAATGTAT 420
 GTGGCATTGA ATGGAAAAGG AGCTCCAAGG AGAGGACAGA AAACACGAAG GAAAAACACC 480
 TCTGCTCACT TTCTTCCAAT GGTGGTACAC TCATAA 516

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser
 1 5 10 15
 Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser
 20 25 30
 Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe
 35 40 45
 Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly Thr
 50 55 60
 Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu
 65 70 75 80
 Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala
 85 90 95
 Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp
 100 105 110
 Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala
 115 120 125
 Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu Asn
 130 135 140
 Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr

145

150

155

160

Ser Ala His Phe Leu Pro Met Val Val His Ser
165 170

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTGCCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTTTC

60

TCGTGTTTTTC TGTCC

75

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC 240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT 300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG 360
AGAGGACAGA AAACACGAGA AAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420
TCATAG 426

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe
1				5					10					15	
Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser
			20					25					30		
Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser
		35					40					45			
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr
	50					55					60				
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn
65				70						75				80	
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr
			85						90					95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala
			100					105					110		
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Glu	Lys
		115					120						125		

Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCTG

60

TCGTGTTTTTC TGTCC

75

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA

60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTCTGGA CCAAGAAGGA GAACTGCCCC 120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC 240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT 300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG 360
AGAGGACAGA AAACACGACA GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420
TCATAG 426

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Gln Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTTTCC TGTCTCTCC TTGG 84

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 426 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC 240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT 300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG 360
AGAGGACAGG AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420
TCATAG 426

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
1 5 10 15
Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
20 25 30
Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
35 40 45
Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
50 55 60
Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
65 70 75 80
Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
85 90 95
Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
100 105 110
Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Glu Thr Arg Arg Lys
115 120 125
Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT

60

TCGTGTCTGC TGTCTCTCC TTGG

84

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA

60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG

120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC

180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC 240
 AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT 300
 AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG 360
 AGAGGACAGC AGACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420
 TCATAG 426

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe	1	5	10	15
Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser	20	25	30	
Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser	35	40	45	
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr	50	55	60	
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn	65	70	75	80
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr	85	90	95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala	100	105	110	
Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Gln	Thr	Arg	Arg	Lys	115	120	125	
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser	130	135	140				

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTTTTTC TGTCTTCCC TTGGAGCTCC TTT 93

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAA AGAATTTAAC 240

AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATT 300
 AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG 360
 GAAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420
 TCATAG 426

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe Ser
 1 5 10 15
 Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly
 20 25 30
 Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val
 35 40 45
 Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu
 50 55 60
 Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn
 65 70 75 80
 Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr
 85 90 95
 Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu
 100 105 110
 Asn Gly Lys Gly Ala Pro Arg Glu Gly Gln Lys Thr Arg Arg Lys Asn
 115 120 125
 Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
 130 135 140

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG 32

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGGAAGAAAG TGAGCAGAGG TGTTTTTCCT 60

TCGTGTTTTTC TGTCCCTGCC TTGGAGCTCC TTT 93

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 426 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA 60

TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG 120

TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAC 180

AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAACTCT ATGGCTCAA AGAATTTAAC 240

AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAATGGAT ACAATACCTA TGCATCATTT 300

AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAAAAGG AGCTCCAAGG 360
 CAGGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC 420
 TCATAG 426

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Met Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys Leu Phe
 1 5 10 15
 Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser
 20 25 30
 Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser
 35 40 45
 Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr
 50 55 60
 Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn
 65 70 75 80
 Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr Asn Thr
 85 90 95
 Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala
 100 105 110
 Leu Asn Gly Lys Gly Ala Pro Arg Gln Gly Gln Lys Thr Arg Arg Lys
 115 120 125
 Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser
 130 135 140

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCGGCACATG TCTTACAACC ACCTGCAGGG TG

32

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGAATGGAG AAGGAGCTCC A

21

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TGGAGCTCCT TCTCCATTCA A

21

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGCCCAAGC TTTTATGAGT GTACCACCAT TGG

33

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ATGTCTTACA ACCACCTGCA GGGTGACGTT CGTTGGCGTA AACTGTTCTC TTTCACCAAA	60
TACTTCCTGA AAATCGAAAA AAACGGTAAA GTTTCTGGGA CCAAGAAGGA GAACTGCCCCG	120
TACAGCATCC TGGAGATAAC ATCAGTAGAA ATCGGAGTTG TTGCCGTCAA AGCCATTAAAC	180
AGCAACTATT ACTTAGCCAT GAACAAGAAG GGGAAACTCT ATGGCTCAAA AGAATTTAAC	240
AATGACTGTA AGCTGAAGGA GAGGATAGAG GAAAATGGAT ACAATACCTA TGCATCATTT	300
AACTGGCAGC ATAATGGGAG GCAAATGTAT GTGGCATTGA ATGGAGAAGG AGCTCCAAGG	360
AGAGGACAGA AAACACGAAG GAAAAACACC TCTGCTCACT TTCTTCCAAT GGTGGTACAC	420
TCATAG	426

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg	Lys	Leu	Phe
1				5					10					15	
Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly	Lys	Val	Ser
			20					25					30		

Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu	Ile	Thr	Ser
		35					40					45			
Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser	Asn	Tyr	Tyr
	50					55					60				
Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys	Glu	Phe	Asn
65					70					75					80
Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly	Tyr	Asn	Thr
			85						90					95	
Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met	Tyr	Val	Ala
			100					105						110	
Leu	Asn	Gly	Glu	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr	Arg	Arg	Lys
	115						120					125			
Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser			
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAAATGAA	240
TCGGCCAACG CGCGGGGAGA GCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GCGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAGGCC	420
AGCAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540

TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTTC CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CTTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGTTTTTTTT GTTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA	1140
CAATTCGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA	1200
ACCTTTCGCG GTATGGCATG ATAGCGCCCC GAAGAGAGTC AATTCAGGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG	1380
ATGGCGGAGC TGAATTACAT TCCAACCGC GTGGCACAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTCGCG	1500
GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTG ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTTCT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG ACTGGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGGCGC GTCTGCGTCT GGCTGGCTGG	1860
CATAAATATC TCACTCGCAA TCAAATTCAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCACTGCG	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GGCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACCAC CATCAAACAG GATTTTCGCC TGCTGGGGCA AACCAGCGTG	2160
GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCCCGTC	2220

TCACTGGTGA	AAAGAAAAAC	CACCCTGGCG	CCCAATACGC	AAACCGCCTC	TCCCCGCGCG	2280
TTGGCCGATT	CATTAATGCA	GCTGGCACGA	CAGGTTTCCC	GA CTGGAAAG	CGGGCAGTGA	2340
GCGCAACGCA	ATTAATGTAA	GTTAGCGCGA	ATTGTGACC	AAAGCGGCCA	TCGTGCCTCC	2400
CCACTCCTGC	AGTTCGGGGG	CATGGATGCG	CGGATAGCCG	CTGCTGGTTT	CCTGGATGCC	2460
GACGGATTTG	CACTGCCGGT	AGAACTCCGC	GAGGTCGTCC	AGCCTCAGGC	AGCAGCTGAA	2520
CCAAC TCGCG	AGGGGATCGA	GCCCCGGGTG	GGCGAAGAAC	TCCAGCATGA	GATCCCCGCG	2580
CTGGAGGATC	ATCCAGCCGG	CGTCCCGGAA	AACGATTCCG	AAGCCCAACC	TTTCATAGAA	2640
GGCGGCGGTG	GAATCGAAAT	CTCGTGATGG	CAGGTTGGGC	GTCGCTTGGT	CGGTCATTTT	2700
GAACCCAGAG	GTCCCGCTCA	GAAGAACTCG	TCAAGAAGGC	GATAGAAGGC	GATGCGCTGC	2760
GAATCGGGAG	CGGCGATACC	GTAAGCACG	AGGAAGCGGT	CAGCCCATTC	GCCGCCAAGC	2820
TCTTCAGCAA	TATCACGGGT	AGCCAACGCT	ATGTCCTGAT	AGCGGTCCGC	CACACCCAGC	2880
CGGCCACAGT	CGATGAATCC	AGAAAAGCGG	CCATTTTCCA	CCATGATATT	CGGCAAGCAG	2940
GCATCGCCAT	GGGTCACGAC	GAGATCCTCG	CCGTCGGGCA	TGCGCGCCTT	GAGCCTGGCG	3000
AACAGTTCCG	CTGGCGCGAG	CCCCTGATGC	TCTTCGTCCA	GATCATCCTG	ATCGACAAGA	3060
CCGGCTTCCA	TCCGAGTACG	TGCTCGCTCG	ATGCGATGTT	TCGCTTGGTG	GTCGAATGGG	3120
CAGGTAGCCG	GATCAAGCGT	ATGCAGCCGC	CGCATTCAT	CAGCCATGAT	GGATACTTTC	3180
TCGGCAGGAG	CAAGGTGAGA	TGACAGGAGA	TCCTGCCCCG	GCACTTCGCC	CAATAGCAGC	3240
CAGTCCCTTC	CCGCTTCAGT	GACAACGTCG	AGCACAGCTG	CGCAAGGAAC	GCCCCGTCGTG	3300
GCCAGCCACG	ATAGCCGCGC	TGCCTCGTCC	TGCAGTTCAT	TCAGGGCACC	GGACAGGTGC	3360
GTCTTGACAA	AAAGAACCGG	GCGCCCCTGC	GCTGACAGCC	GGAACACGGC	GGCATCAGAG	3420
CAGCCGATTG	TCTGTTGTGC	CCAGTCATAG	CCGAATAGCC	TCTCCACCCA	AGCGGCCGGA	3480
GAACCTGCGT	GCAATCCATC	TTGTTCAATC	ATGCGAAACG	ATCCTCATCC	TGTCTCTTGA	3540
TCAGATCTTG	ATCCCCTGCG	CCATCAGATC	CTTGGCGGCA	AGAAAGCCAT	CCAGTTTACT	3600
TTGCAGGGCT	TCCCAACCTT	ACCAGAGGGC	GCCCCAGCTG	GCAATTCCGG	TTGCTTGGCT	3660
GTCCATAAAA	CCGCCCAGTC	TAGCTATCGC	CATGTAAGCC	CACTGCAAGC	TACCTGCTTT	3720
CTCTTTGCGC	TTGCGTTTTT	CCTTGTCAG	ATAGCCCAGT	AGCTGACATT	CATCCGGGGT	3780
CAGCACCGTT	TCTGCGGACT	GGCTTTCTAC	GTGTTCCGCT	TCCTTTAGCA	GCCCTTGCGC	3840
CCTGAGTGCT	TGCGGCAGCG	TGAAGCTTAA	AAAAGTGCAA	AAAATAGTTT	GACTTGTGAG	3900

10075445.034303

CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTCACAC ATTAAAGAGG 3960
AGAAATTACA TATG 3974

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC 60
CAATTGTGAG CGGATAACAA TTTACACAT TAAAGAGGAG AAATTACATA TG 112